WE CLAIM:

1. A nucleic acid which is replicatable in a microorganism of the family Corynebacterium and optionally a recombinant nucleic acid, characterized in that it has a nucleotide sequence coding for L-serine dehydratase which is partially or completely mutated or expressed to a lesser degree than the naturally occuring nucleotide sequence or which is not expressed at all.

2. A nucleic acid according to claim 1, characterized in that the *sdaA* gene sequence is partially or completely deleted or mutated or expressed to a lesser extent by comparison with the naturally occuring sequence or not expressed at all.

3. A nucleic acid according to one of claims 1 to 2, characterized by a nucleotide sequence according to SEQ ID NO 1 whose nucleotides form position 506 to position 918 are completely or partially deleted or mutated, or an allele, homolog or derivative of this nucleotide sequence or a nucleotide sequence hybridizing therewith.

4. A nucleic acid according to one of claims 1 to 3, characterized in that it is isolated from a coryneform bacterium.

5. A nucleic acid according to one of claims 1 to 4, characterized in that it is isolated from Corynbacterium or Brevibacterium.

6. A nucleic acid according to one of claims 1 to 5, characterized in that it is isolated from *Corynebacterium glutamicim* or *Brevibacterium flavum*.

7. A gene structure containing at least one nucleotide sequence according to claims 1 to 6 and nucleotide sequences having regulatory sequences operatively linked therewith.

8. A vector containing at least one nucleotide sequence according to claims 1 to 6 or a gene structure according to claim 7 and additional nucleotide sequences for selection, for replication in the host cell or for integration in the host cell genone.

9. L-serine dehydratase with reduced L-serine dehydratase activity coded with a nucleic acid according to one of claims 1 to 6.

10. L-serine dehydratase according to claim 9 with an amino acid sequence according to sequence ID 2 whose amino acid are altered in positions 135 to 274 or a modified form of this polypeptide sequence or an isoform thereof.

11. L-serine dehydratase according to one of claims 9 to 10, characterized in that it derives from coryneform bacteria.

12. L-serine dehydratase according to one of claims 9 to 10, characterized in that it derives from coryneform bacteria or brevibacteria.

13. L-serine dehydratase according to one of claims 9 to 12, characterized in that it derives from *Corynebacterium glutamicum* or *Brevibacterium flavum*.

14. A microorganism characterized in that it has a nucleotide sequence which codes for an L-serine dehydratase, which is deleted in whole or in part or is mutated or is expressed to a reduced extent by comparison with the naturally occuring nucleotide sequence or is not expressed at all.

15. A microorganism according to claim 14, characterized in that its *sdaA* gene is wholly or partially deleted or mutated or to a reduced extent by comparison with the naturally occuring *sdaA* gene or is not expressed at all.

16. A microorganism according to one of claims 14 to 15 containing in replicatable form a nucleic acid according to one of

claims 1 to 6, a gene structure according to claim 7, a vector according to claim 8 or a polypeptide according to claims 9 to 14.

17. A microorganism according to one of claims 14 to 16, characterized in that it is a coryneform bacteria.

18. A microorganism according to one of claims 14 to 17, characterized in that it brings to the family a coryneform bacteria or brevibacteria.

19. A microorganism according to one of claims 14 to 18, characterized in that it brings to the family a *Corynebacterium glutamicum* or *Brevibacterium flavum*.

20. A probe for identifying and/or genes for coding which participate in the biosynthesis of L-serine chacacterized in that they are produced starting with nucleic acids according to one of claims 1 to 6 and contain a suitable marker for detection.

21. A method for the microbial production of L-serine characterized in that

(a) a genetically altered microorganism is produced in which the nucleic acid in the microorganism coding for the L-serine dehydratase is partially or completely deleted or mutated or expressed to a reduced extent by comparison with the naturally occuring nucleic acid or is not expressed at all,

(b) this genetically altered microorganism from step (a) is used for microbial production, and

(c) the L-serine formed is isolated from the culture medium.

22. The method according to claim 21, characterized in that the *sdaA* gene sequence is partially or completely deleted or mutated or expressed to a reduced extent by comparison with the naturally occuring nucleotide sequence or is not expressed at all.

23. The method according to one of claims 21 to 22, characterized in that the nucleotide according to Sequence ID NO 1 is completely or partially deleted or mutated from position 506 to 918 or expressed to a reduced extent by comparison with the naturally occuring nucleotide sequence or not expressed at all.

24. The method according to one of claims 21 to 23, characterized in that a microorganism from the group of Corynebacterium, Brevibacterium, Arthobacter, Pseudomonas, Nocardia, Methylobacteria, Hyphomicrobium, Alkaligenes or Klebsiella is used.

25. The method according to one of claims 21 to 24, characterized in that a nucleic acid according to claims 1 to 6 a gene structure according to claim 7 or a vector according to claim 8 is used.

Amended